```
=> s transaldolase/cn
L1             1 TRANSALDOLASE/CN

=> d

L1   ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2003 ACS
RN   9014-46-4  REGISTRY
CN   Transaldolase (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   Dihydroxyacetonetransferase
CN   E.C. 2.2.1.2
MF   Unspecified
CI   MAN
LC   STN Files:   AGRICOLA, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CABA, CAPLUS,
       CHEMCATS, CHEMLIST, EMBASE, TOXCENTER, USPAT2, USPATFULL
     Other Sources:   EINECS**
         (**Enter CHEMLIST File for up-to-date regulatory information)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
             437 REFERENCES IN FILE CA (1957 TO DATE)
               2 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
             438 REFERENCES IN FILE CAPLUS (1957 TO DATE)
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=> d his

     (FILE 'HOME' ENTERED AT 15:23:58 ON 08 JUL 2003)

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L1             1 S TRANSALDOLASE/CN

     FILE 'HCAPLUS' ENTERED AT 15:25:27 ON 08 JUL 2003

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L2           SEL L1 1- CHEM :        4 TERMS
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     FILE 'HCAPLUS' ENTERED AT 15:25:33 ON 08 JUL 2003
L3           664 S L2
L4             4 S L3 (L) (CORYNEBACTERIA OR CORYNEBACTERIA GLUTAMICUM OR (BACTE
```

=> d ibib ab 1-4

L4 ANSWER 1 OF 4 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:246415 HCAPLUS
DOCUMENT NUMBER: 135:328890
TITLE: Modeling and Experimental Design for Metabolic Flux Analysis of Lysine-Producing Corynebacteria by Mass Spectrometry
AUTHOR(S): Wittmann, Christoph; Heinzle, Elmar
CORPORATE SOURCE: Biochemical Engineering Institute, Saarland University, Saarbruecken, Germany
SOURCE: Metabolic Engineering (2001), 3(2), 173-191
CODEN: MEENFM; ISSN: 1096-7176
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Exptl. design of 13C-tracer studies for metabolic flux anal. with mass spectrometric detn. of labeling patterns was performed for the central metab. of Corynebacterium glutamicum comprising various flux scenarios. Ratio measurement of mass isotopomer pools of Corynebacterium products lysine, alanine, and trehalose is sufficient to quantify the flux partitioning ratios (i) between glycolysis and pentose phosphate pathways (.PHI.PPP), (ii) between the split pathways in the lysine biosynthesis (.PHI.DH), (iii) at the pyruvate node (.PHI.PC), and the reversibility of (iv) glucose 6-phosphate isomerase (.zeta.PGI), (v) at the pyruvate node (.zeta.PC/PEPCK), and (vi) of transaldolase and transketolases in the PPP. Weighted sensitivities for flux parameters were derived from partial derivs. to quant. evaluate exptl. approaches and predict precision for estd. flux parameters. Deviation of intensity ratios from ideal values of 1 was used as weighting function. Weighted flux sensitivities can be used to identify optimal type and degree of tracer labeling or potential intensity ratios to be measured. Exptl. design for lysine-producing strain C. glutamicum MH 20-22B and various potential mutants with different alterations in the flux pattern showed that specific tracer labeling is optimal to quantify a certain flux parameter uninfluenced by the overall flux situation. Identified substrates of choice are [1-13C]glucose for the estn. of .PHI.PPP and .zeta.PGI and a 1:1 mixt. of [U-12C/U-13C]glucose for the detn. of .zeta.PC/PEPCK. .PHI.PC Can be quantified by feeding [4-13C]glucose or [U-12C/U-13C]glucose (1:1), whereas .PHI.DH is accessible via [4-13C]glucose. The sensitivity for the quantification of a certain flux parameter can be influenced by superposition through other flux parameters in the network, but substrate and measured mass isotopomers of choice remain the same. In special cases, reduced labeling degree of the tracer substrate can increase the precision of flux anal. Enhanced precision and flux information can be achieved via multiply labeled substrates. The presented approach can be applied for effective exptl. design of 13C tracer studies for metabolic flux anal. Intensity ratios of other products such as glutamate, valine, phenylalanine, and riboflavin also sensitively reflect flux parameters, which underlines the great potential of mass spectrometry for flux anal. (c) 2001 Academic Press.
REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 4 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:50828 HCAPLUS
DOCUMENT NUMBER: 134:111274
TITLE: Sequences of Coryneform bacteria tal gene and uses thereof in fermentative preparation of L-amino acids
INVENTOR(S): Dunican, L. K.; McCormack, Ashling; Stapelton, Cliona; Burke, Kevin; Mockel, Bettina
PATENT ASSIGNEE(S): Degussa-Huls Aktiengesellschaft, Germany; National University of Ireland
SOURCE: PCT Int. Appl., 47 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001004325	A1	20010118	WO 2000-EP6304	20000705
W: AU, BR, CA, CN, HU, ID, JP, KR, MX, PL, RU, SK, UA, ZA				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
EP 1109915	A1	20010627	EP 2000-956165	20000705
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
BR 2000006915	A	20010731	BR 2000-6915	20000705

PRIORITY APPLN. INFO.: US 1999-142915P P 19990709
US 2000-531266 A 20000320
WO 2000-EP6304 W 20000705

AB The invention provides protein and DNA sequences of tal genes from coryneform bacteria. The invention further provides new measures for improved fermentative prepn. of amino acids, in particular L-lysine, L-threonine, L-isoleucine and L-tryptophan.

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 4 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:50825 HCAPLUS
DOCUMENT NUMBER: 134:111273
TITLE: Sequences of Coryneform bacteria opcA gene and uses thereof in fermentative preparation of L-amino acids
INVENTOR(S): Dunican, L. K.; McCormack, Ashling; Stapelton, Cliona; Burke, Kevin; Moritz, Bernd; Eggeling, Lothar; Sahm, Hermann; Mockel, Bettina; Weissenborn, Anke
PATENT ASSIGNEE(S): Degussa-Huls Aktiengesellschaft, Germany; Forschungszentrum Julich G.m.b.H.; National University of Ireland
SOURCE: PCT Int. Appl., 75 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001004322	A1	20010118	WO 2000-EP6300	20000705
WO 2001004322	C2	20020912		
W: AU, BR, CA, CN, HU, ID, JP, KR, MX, PL, RU, SK, UA, ZA				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
BR 2000006909	A	20010612	BR 2000-6909	20000705
EP 1109913	A1	20010627	EP 2000-945874	20000705
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRIORITY APPLN. INFO.: US 1999-142915P P 19990709
US 2000-531267 A 20000320
WO 2000-EP6300 W 20000705

AB The invention provides protein and DNA sequences of opcA genes from coryneform bacteria. The invention further provides new measures for improved fermentative prepn. of amino acids, in particular L-lysine, L-threonine, L-isoleucine and L-tryptophan.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 4 OF 4 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1962:26672 HCAPLUS
DOCUMENT NUMBER: 56:26672
ORIGINAL REFERENCE NO.: 56:5110h-i
TITLE: Pentose cycle in Corynebacterium diphtheriae
AUTHOR(S): Halanicka, Danuta
CORPORATE SOURCE: Inst. Mother Child, Warsaw, Polish
SOURCE: Acta Biochimica Polonica (1960), 7, 449-57

CODEN: ABPLAF; ISSN: 0001-527X
DOCUMENT TYPE: Journal
LANGUAGE: Unavailable
AB Enzymes of the pentose cycle in Me2CO powder exts. and in the supernatants (18,500 g, 30 min.) of Corynebacterium diphtheriae were investigated. The prepns. metabolized ribose 5-phosphate and produced keto sugars. Identification of ribose 5-phosphate was performed speetrophotometrically by means of the Dische reaction. Formation of sedoheptulose and its transition into hexose was shown. The presence of the following enzymes in **Corynebacteria** was found: phosphopentose isomerase, epimerase, transketolase, **transaldolase**, glucose-6-phosphate dehydrogenase, 6-phosphogluconic acid dehydrogenase, and ribokinase. Dehydrogenases were linked with triphosphopyridine nucleotide, the kinase was specific for ribose.

RESULT 4
AAF25333
ID AAF25333 standard; DNA; 1083 BP.
XX
AC AAF25333;
XX
DT 30-APR-2001 (first entry)
XX
DE Coding region of the tal gene.
XX
KW tal gene; Coryneform bacteria; L-amino acid; transaldolase; ss.
XX
OS Corynebacterium glutamicum.
XX
FH Key   Location/Qualifiers
FT CDS   1..1083
FT   /*tag= a
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PN WO200104325-A1.
XX
PD 18-JAN-2001.
XX
PF 05-JUL-2000; 2000WO-EP06304.
XX
PR 09-JUL-1999; 99US-0142915.
PR 20-MAR-2000; 2000US-0531266.
XX
PA (DEGS) DEGUSSA-HUELS AG.
PA (UYNA-) UNIV NAT IRELAND.
XX
PI Dunican LK, McCormack A, Stapelton C, Burke K, Moeckel B;
XX
DR WPI; 2001-159407/16.
DR P-PSDB; AAB31783.
XX
PT New polynucleotides from coryneform bacteria, specifically
PT Corynebacterium, useful for preparing L-amino acids, especially
PT L-lysine, L-threonine, L-isoleucine and L-tryptophan, by amplifying tal
PT gene -
XX
PS Claim 4; Page 43-45; 48pp; English.
XX
CC The present sequence represents a tal gene fragment from Coryneform
CC bacteria. Tal polynucleotides and polypeptides are used for fermentative
CC preparation of L-amino acids, especially L-lysine, L-threonine,
CC L-isoleucine and/or L-tryptophan. The tal polynucleotide is useful as
CC a hybridisation probe for isolating a cDNA encoding for the tal gene
CC product, and for isolating cDNA or genes having high similarity with
CC the sequence of the tal gene. The polynucleotides may be used as
CC hybridisation probes for RNA, cDNA and DNA to isolate full-length cDNA
CC which code for transaldolase and to isolate those cDNA or genes, which
CC have a high similarity with that of the transaldolase gene. These may
CC also be used as primers for the preparation of DNA which code for
CC transaldolase by polymerase chain reaction (PCR).
XX
SQ Sequence 1083 BP; 215 A; 336 C; 294 G; 238 T; 0 other;

Query Match 98.7%; Score 1065.6; DB 22; Length 1083;
Best Local Similarity 99.2%; Pred. No. 1e-269;
Matches 1071; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy         61 CGCGAGCGCATTACTTCCGGCAATCTCAGCCAGGTTATTGAGGAAAAGTCTGTAGTCGGT 120
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Db         61 CGCGAGCGCATTACTTCCGGCAATCTCAGCCAGGTTATTGAGGAAAAGTCTGTAGTCGGT 120

Qy        121 GTCACCACCAACCCAGCTATTTTCGCAGCAGCAATGTCCAAGGGCGATTCCTACGACGCT 180
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Qy        181 CAGATCGCAGAGCTCAAGGCCGCTGGCGCATCTGTTGACCAGGCTGTTTACGCCATGAGC 240
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Db        301 TACGACGGCCGCGTGTCCATCGAGGTTGACCCACGTATCTCTGCTGACCGCGACGCAACC 360

Qy        361 CTGGCTCAGGCCAAGGAGCTGTGGGCAAAGGTTGATCGTCCAAACGTCATGATCAAGATC 420
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Qy        421 CCTGCAACCCCAGGTTCTTTGCCAGCAATCACCGACGCTTTGGCTGAGGGCATCAGCGTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        481 AACGTCACCTTGATCTTCTCCGTTGCTCGCTACCGCGAGGTCATCGCTGCGTACATCGAG 540
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Qy        541 GGAATCAAGCAGGCAGCTGCAAACGGCCACGACGTATCCAAGATCCACTCTGTGGCTTCC 600
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Qy        661 GAGGCTTTGGCTCTGCGCGGCAAGGCAGGCGTTGCCAACGCTCAGCGCGCTTACGCTGTG 720
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Db        721 TACAAGGAGCTTTTCGACGCCGCCGAGCTGCCTGAAGGTGCCAACACTCAGCGCCCACTG 780
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Qy 1021 GTGGACAAGTTTGTTGCTTCTTGGAGCGAACTGCTTGAGTCCATGGAAGCTCGCCTGAAG 1080
Db 1021 GTGGACAAGTTCGTTGCTTCTTGGAGCGAACTGCTTGAGTCCATGGAAGCTCGCCTGAAG 1080

RESULT 4
AAF25333
ID AAF25333 standard; DNA; 1083 BP.
XX
AC AAF25333;
XX
DT 30-APR-2001 (first entry)
XX
DE Coding region of the tal gene.
XX
KW tal gene; Coryneform bacteria; L-amino acid; transaldolase; ss.
XX
OS Corynebacterium glutamicum.
XX
FH Key   Location/Qualifiers
FT CDS   1..1083
FT   /*tag= a
FT   /product= "tal"
XX
PN WO200104325-A1.
XX
PD 18-JAN-2001.
XX
PF 05-JUL-2000; 2000WO-EP06304.
XX
PR 09-JUL-1999;   99US-0142915.
PR 20-MAR-2000; 2000US-0531266.
XX
PA (DEGS) DEGUSSA-HUELS AG.
PA (UYNA-) UNIV NAT IRELAND.
XX
PI Dunican LK, McCormack A, Stapelton C, Burke K, Moeckel B;
XX
DR WPI; 2001-159407/16.
DR P-PSDB; AAB31783.
XX
PT New polynucleotides from coryneform bacteria, specifically
PT Corynebacterium, useful for preparing L-amino acids, especially
PT L-lysine, L-threonine, L-isoleucine and L-tryptophan, by amplifying tal
PT gene -
XX
PS Claim 4; Page 43-45; 48pp; English.
XX
CC The present sequence represents a tal gene fragment from Coryneform
CC bacteria. Tal polynucleotides and polypeptides are used for fermentative
CC preparation of L-amino acids, especially L-lysine, L-threonine,
CC L-isoleucine and/or L-tryptophan. The tal polynucleotide is useful as
CC a hybridisation probe for isolating a cDNA encoding for the tal gene
CC product, and for isolating cDNA or genes having high similarity with
CC the sequence of the tal gene. The polynucleotides may be used as
CC hybridisation probes for RNA, cDNA and DNA to isolate full-length cDNA
CC which code for transaldolase and to isolate those cDNA or genes, which
CC have a high similarity with that of the transaldolase gene. These may
CC also be used as primers for the preparation of DNA which code for
CC transaldolase by polymerase chain reaction (PCR).
XX
SQ Sequence 1083 BP; 215 A; 336 C; 294 G; 238 T; 0 other;

Query Match 98.7%; Score 1065.6; DB 22; Length 1083;
Best Local Similarity 99.2%; Pred. No. 1e-269;
Matches 1071; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy        541 GGAATCAAGCAGGCAGCTGCAAACGGCCACGACGTATCCAAGATCCACTCTGTGGCTTCC 600
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